

SEQUENCE LISTING

<110> Kazuko, SHINOZAKI  
Mie, KASUGA

<120> Environmental Stress-Tolerant Plants

<130> 382.1029DIV2

<150> JP292348/1998  
US 09/301,217

<151> 1998-10-14  
1999-04-28

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<170> PatentIn Ver. 2.0

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atg aac tca ttt tct gct ttt tct gaa atg ttt ggc tcc gat tac gag 166  
Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu  
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tct tcg gtt tcc tca ggc ggt gat tat att ccg acg ctt gcg agc agc 214  
Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser  
20 25 30  
tgc ccc aag aaa ccg gcg ggt cgt aag aag ttt cgt gag act cgt cac 262  
Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His  
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cca ata tac aga gga gtt cgt ccg aga aac tcc ggt aag tgg gtt tgt 310  
Pro Ile Tyr Arg Gly Val Arg Arg Asn Ser Gly Lys Trp Val Cys  
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gag gtt aga gaa cca aac aag aaa aca agg att tgg ctc gga aca ttt 358  
Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe  
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caa acc gct gag atg gca gct cga gct cac gac gtt gcc gct tta gcc 406  
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala  
85 90 95  
ctt cgt ggc cga tca gcc tgt ctc aat ttc gct gac tcg gct tgg aga 454  
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg  
100 105 110  
ctc cga atc ccg gaa tca act tgc gct aag gac atc caa aag gcg gcg 502  
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala  
115 120 125  
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165	170	175	
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Asp Asp Val Ser Leu Trp Ser Tyr			
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Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr			
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Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe			
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Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro			
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tat gat cag agt gga gat aga aac aga aca caa att gat aca tcg agg 223  
Tyr Asp Gln Ser Gly Asp Arg Asn Arg Thr Gln Ile Asp Thr Ser Arg  
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aaa agg aaa tct aga agt aga ggt gac ggt act act gtg gct gag aga 271  
Lys Arg Lys Ser Arg Ser Arg Gly Asp Gly Thr Thr Val Ala Glu Arg  
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Leu Lys Arg Trp Lys Glu Tyr Asn Glu Thr Val Glu Glu Val Ser Thr  
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Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys Met Lys  
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Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Arg  
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Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln Glu Ala Ala  
100 105 110 115  
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Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro Leu Ala Arg  
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ctt aat ttc cct cgg tct gat gcg tct gag gtt acg agt acc tca agt 607  
Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser Thr Ser  
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Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val His Val Lys  
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Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly Gly Val Glu  
165 170 175  
ccg atg tat tgt ctg gag aat ggt gcg gaa gag atg aag aga ggt gtt 751  
Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys Arg Gly Val  
180 185 190 195  
aaa gcg gat aag cat tgg ctg agc gag ttt gaa cat aac tat tgg agt 799  
Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn Tyr Trp Ser  
200 205 210  
gat att ctg aaa gag aaa gag aac cag aag gag caa ggg att gta gaa 847  
Asp Ile Leu Lys Glu Lys Glu Lys Gln Lys Glu Gln Gly Ile Val Glu  
215 220 225  
acc tgt cag caa caa cag cag gat tcg cta tct gtt gca gac tat ggt 895  
Thr Cys Gln Gln Gln Gln Asp Ser Leu Ser Val Ala Asp Tyr Gly

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Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp Val Phe Ala			
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Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala Asn Gly Ser			
280	285	290	
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tgtatatac gaaacagtga tatgacaata gagaagacaa ctatagttt tagtctgct			1361
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Cys Met Lys Gly Lys Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg			
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Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu			
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Leu Ala Arg Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser			
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Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val			
145	150	155	160
His Val Lys Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly			
165	170	175	
Gly Val Glu Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys			
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Arg Gly Val Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn			
195	200	205	

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 210 215 220  
 Ile Val Glu Thr Cys Gln Gln Gln Gln Asp Ser Leu Ser Val Ala  
 225 230 235 240  
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 Asp Met Phe Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp  
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 Met Asn Ser Phe  
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 Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu Pro Gln Gly Gly  
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 25 30 35  
 cgt aag aag ttt cgt gag act cgt cac cca att tac aga gga gtt cgt 319  
 Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg  
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 caa aga aac tcc ggt aag tgg gtt tct gaa gtg aga gag cca aac aag 367  
 Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg Glu Pro Asn Lys  
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 aaa acc agg att tgg ctc ggg act ttc caa acc gct gag atg gca gct 415  
 Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala  
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 Arg Ala His Asp Val Ala Ala Leu Arg Gly Arg Ser Ala Cys  
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 Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr  
 105 110 115  
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 Cys Ala Lys Asp Ile Gln Lys Ala Ala Glu Ala Ala Leu Ala Phe  
 120 125 130  
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165	170	175	180
gat aat atg gct gaa ggc atg ctt tta ccg ccg ccg tct gtt caa tgg			751
Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Ser Val Gln Trp			
185	190	195	
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Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val Ser Leu Trp Ser			
200	205	210	
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Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala			
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Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly			
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Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile			
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Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala			
115	120	125	
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Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met			
165	170	175	
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Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly  
1 5 10  
tcc gat tac gag tct ccg gtt tcc tca ggc ggt gat tac agt ccg aag 218  
Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys  
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Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg  
30 35 40  
gag act cgt cac cca att tac aga gga gtt cgt caa aga aac tcc ggt 314  
Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly  
45 50 55 60  
aag tgg gtg tgt gag ttg aga gag cca aac aag aaa acg agg att tgg 362  
Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp  
65 70 75  
ctc ggg act ttc caa acc gct gag atg gca gct cgt gct cac gac gtc 410  
Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val  
80 85 90  
gcc gcc ata gct ctc cgt ggc aga tct gcc tgt ctc aat ttc gct gac 458  
Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp  
95 100 105  
tcg gct tgg cgg cta cga atc ccg gaa tca acc tgt gcc aag gaa atc 506  
Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile  
110 115 120  
caa aag gcg gcg gct gaa gcc gcg ttg aat ttt caa gat gag atg tgt 554  
Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys  
125 130 135 140  
cat atg acg acg gat gct cat ggt ctt gac atg gag gag acc ttg gtg 602  
His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val  
145 150 155  
gag gct att tat acg ccg gaa cag agc caa gat gcg ttt tat atg gat 650  
Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp  
160 165 170  
gaa gag gcg atg ttg ggg atg tct agt ttg gat aac atg gcc gaa 698  
Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu  
175 180 185  
ggg atg ctt tta ccg tcg ccg tcg gtt caa tgg aac tat aat ttt gat 746  
Gly Met Leu Leu Pro Ser Pro Val Gln Trp Asn Tyr Asn Phe Asp  
190 195 200  
gtc gag gga gat gat gac gtg tcc tta tgg agc tat taaaattcga 792  
Val Glu Gly Asp Asp Val Ser Leu Trp Ser Tyr  
205 210 215  
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50 55 60  
Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe  
65 70 75 80  
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala  
85 90 95  
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg  
100 105 110  
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala  
115 120 125  
Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr  
130 135 140  
Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr  
145 150 155 160  
Thr Pro Clu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met  
165 170 175  
Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu  
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cgactcta at cctggagttt tcattcacga tagattctta gattgcgact ataaagaaga 180  
ag atg gct gta tat gaa caa acc gga acc gag cag ccg aag aaa agg 227  
Met Ala Val Tyr Glu Gln Thr Gly Thr Glu Gln Pro Lys Lys Arg  
1 5 10 15  
aaa tct agg gct cga gca ggt ggt tta acg gtg gct gat agg cta aag 275  
Lys Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys  
20 25 30  
aag tgg aaa gag tac aac gag att gtt gaa gct tcg gct gtt aaa gaa 323  
Lys Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu  
35 40 45  
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Gly Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly

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Cys Met Lys Gly Lys Gly Gly Pro Asp Asn Ser His Cys Ser Phe Arg			
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gga gtt aga caa agg att tgg ggt aaa tgg gtt gca gag att cga gaa			467
Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu			
80	85	90	95
ccg aaa ata gga act aga ctt tgg ctt ggt act ttt cct acc gcg gaa			515
Pro Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu			
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aaa gct gct tcc gct tat gat gaa gcg gct acc gct atg tac ggt tca			563
Lys Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser			
115	120	125	
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Leu Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser			
130	135	140	
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Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val			
145	150	155	
tgt ggt gat gtt tgg aag cat gaa gat act gat tgg gaa tct aat			707
Cys Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn			
160	165	170	175
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Pro Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg			
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Tyr Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu			
210	215	220	
cag gag aaa gag aaa ccg aag cag gaa gaa gag gag ata cag caa cag			899
Gln Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Glu Ile Gln Gln Gln			
225	230	235	
caa cag gaa cag caa cag ctt ctt ctt act gtt			947
Gln Gln Glu Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val			
240	245	250	255
gca gat tac ggt tgg cct tgg tct aat gat att gta aat gat cag act			995
Ala Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr			
260	265	270	
tct tgg gat cct aat gag tgc ttt gat att aat gaa ctc ctt gga gat			1043
Ser Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp			
275	280	285	
ttg aat gaa cct ggt ccc cat cag agc caa gac caa aac cac gta aat			1091
Leu Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn			
290	295	300	
tct ggt agt tat gat ttg cat ccc ctt cat ctc gag cca cac gat ggt			1139
Ser Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly			
305	310	315	
cac gag ttc aat ggt ttg agt tct ctg gat att tgagagttct gaggcaatgg	1192		
His Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile			
320	325	330	
tcctacaaga ctacaacata atctttggat tgatcatagg agaaaacaaga aataggtgtt	1252		
aatgatctga ttccacaatga aaaaatattt aataactcta tagttttgt tctttccttg	1312		
gatcatgaac tggcttct catctattga gttatatag cgaatagcag agtttcttc	1372		

tttcttctct ttgttagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaayh sakmabgcar 1432  
srcsdvsnna nntrnatnar sarchcntrr agrctrascn csrcaswash tskbabarak 1492  
aantamaysa kmasrpngna c 1513

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<211> 330  
<212> PRT  
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Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys Lys  
20 25 30  
Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu Gly  
35 40 45  
Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys  
50 55 60  
Met Lys Gly Lys Gly Pro Asp Asn Ser His Cys Ser Phe Arg Gly  
65 70 75 80  
Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro  
85 90 95  
Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu Lys  
100 105 110  
Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser Leu  
115 120 125  
Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser Thr  
130 135 140  
Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val Cys  
145 150 155 160  
Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn Pro  
165 170 175  
Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg Pro  
180 185 190  
Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr  
195 200 205  
Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln  
210 215 220  
Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Ile Gln Gln Gln Gln  
225 230 235 240  
Gln Glu Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala  
245 250 255  
Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser  
260 265 270  
Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp Leu  
275 280 285  
Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn Ser  
290 295 300  
Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly His  
305 310 315 320  
Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile  
325 330

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<212> DNA  
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<220>  
<223> Designed oligonucleotide based on the promoter region of rd29A  
gene and having HindIII site.

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aagcttaagc ttacatcagt ttgaaagaaa 30

<210> 12  
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<223> Designed oligonucleotide based on the promoter region of rd29A  
gene and having HindIII site.

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aagcttaagc ttgcttttg gaactcatgt c 31

<210> 13  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide based on DREB1A gene and having BamHI  
site.

<400> 13  
aagcttaagc ttgccataga tgcaattcaa tc 32  
<210> 14  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide based on DREB1A gene and having BamHI  
site.

<400> 14  
aagcttaagc ttttccaaag attttttct ttccaa 36

<210> 15  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide based on the promoter region of rd29A  
gene and having HindIII site.

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ggatccggat ccatgaactc attttctgct 30

<210> 16

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 16

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32

<210> 17

<211> 941

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<213> Arabidopsis thaliana

<400> 17

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cttatataca ttatattgtt atttttgtt acaaaatgtt ttatttatta ttatagaatt 180  
ttactggta aataaaaat gaatagaaaa ggtgaattaa gaggagagag gaggtaaaca 240  
tttcttcata tttttcata ttttcaggat aaattattgtt aaaagtttac aagatttcca 300  
tttgactagt gtaaatgagg aatattctt agtaagatca ttatccatc tacttcttt 360  
atcttctacc agtagaggaa taaacaatat ttagctcctt tgtaataaca aattaatttt 420  
cattcttgcac atcattcaat ttaattttt cgtataaaat aaaagatcat acctattaga 480  
acgattaagg agaaatacaa ttcaatgag aaggatgttc cgtttgttat aataaacagg 540  
cacacgacgt aaacgtaaaa tgaccacatg atggccaat agacatggac cgactactaa 600  
taatagtaag ttacattttt ggtatggata aatatcatac cgacatcagt tttgaaagaa 660  
aaggaaaaaa aagaaaaaaat aaataaaaaga tatactaccg acatgagttc caaaaagcaa 720  
aaaaaaagat caagccgaca cagacacgctg tagagagcaa aatgactttt acgtcacacc 780  
acgaaaacag acgcttcata cgtgtccctt tatctcttc agtctctcta taaacttagt 840  
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gggttgatt acttcttattt gaaagaaaaaa aatctttgga a 941

<210> 18

<211> 71

<212> DNA

<213> Arabidopsis thaliana

<400> 18

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ttccaaaaag c 71

<210> 19

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 19

cagttgaaa gaaaaggaa aaaaagaaaa aataaataaa agatataattt tcgacatgag 60  
ttccaaaaag c 71

<210> 20

<211> 71

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 20  
cagtttggaaa gaaaaggaa aaaaagaaaa aataaataaa agatatacta cttttatgag 60  
ttccaaaaag c 71

<210> 21  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 21  
cagtttggaaa gaaaaggaa aaaaagaaaa aataaataaa agatatacta ccgacaaaag 60  
ttccaaaaag c 71

<210> 22  
<211> 71  
<212> DNA  
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<220>  
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 22  
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caacaaaaag c 71

<210> 23  
<211> 71  
<212> DNA  
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<220>  
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 23  
cagtttggaaa gaaaaggaa aaaaagaaaa aataaataaa agatatacta ccgacatgag 60  
ttcggttaag c 71